

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Nucleotide sequences which code for the dead gene

<130> 000557 BT

<140>

10 <141>

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2381

<212> DNA

20 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (259) .. (2130)

<223> dead gene

25 <400> 1

caggaaaccc cgcagggtga ctcagcatca getgacttcg ctctcgaac cccaaccaac 60

actgttgaag atgcaccagc atctgagggt agcgaagaga tcaccagggt tgcggatact 120

30 tctgaggacg ccgactctgc agatgcagac aacgcgagca atgtaataca tgagaatgag 180

gactcctcgg aagggtgctaa ccagccttca aacgagtcac cctctacgga agccaaatcc 240

35 ggcttcgatg cactcgga ctg cca gag cgt gta ctt gac gct gtg cgc aag 291

Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys
1 5 10

40 gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc cca atc 339

Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile
15 20 25

ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt acc ggt 387

45 Leu Met 30 Gly Gln Asp 35 Val Val Gly Leu Ala Gln Thr Gly Thr Gly 40

aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac aag tcc 435

Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser
45 50 55

50 gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag cag gca 483

Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala
60 65 70 75

55 ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc ggt ggc 531

Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly
80 85 90

ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att cag ctc 579
 Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu
 95 100 105

5 tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca ggc cga 627
 Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro Gly Arg
 110 115 120

10 atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga ctg cgc 675
 Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg
 125 130 135

15 ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc ttc cag 723
 Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln
 140 145 150 155

20 gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag cag gtt 771
 Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val
 160 165 170

25 gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg tcc aag 819
 Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys
 175 180 185

30 cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag acc agg 867
 Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg
 190 195 200

35 act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac cgc aac 915
 Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn
 205 210 215

40 aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt gaa gca 963
 Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala
 220 225 230 235

45 atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt gct gaa 1011
 Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu
 240 245 250

50 aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc gac att 1059
 Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile
 255 260 265

55 gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac ggc cgc 1107
 Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg
 270 275 280

60 ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt gac gtt 1155
 Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val
 285 290 295

65 gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac acc gag 1203
 Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu
 300 305 310 315

70 tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt acc ggc 1251
 Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly
 320 325 330

5 gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt cgc tcc 1299
 Glu Ala Ile 335 Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser 340 345

atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg cca acc 1347
 Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr 350 355 360

10 gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gct gac tcc atc 1395
 Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile 365 370 375

15 acc aag tcc ctg gag gac aag cag atg gac ctg ttc cgc acc ctg gtc 1443
 Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val 380 385 390 395

20 aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc gca cgc 1491
 Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala 400 405 410

25 gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctg aag gag ctg 1539
 Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu 415 420 425

30 cca cca gag cgc cgt gag cgc aac gac cgc cgt cgt gac cgt gac ttc 1587
 Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe 430 435 440

35 gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac cgc gga 1635
 Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly 445 450 455

gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca acc tac 1683
 Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr 460 465 470 475

40 cgc ctg gca gtg ggc aag cgc cag cac atc cgc cca ggc gca atc gtt 1731
 Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val 480 485 490

45 ggt gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc ggc cgc 1779
 Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg 495 500 505

atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag gat ctg 1827
 Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu 510 515 520

50 cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc ggc cag 1875
 Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln 525 530 535

55 ctg atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc cgc ttc 1923
 Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe 540 545 550 555

gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac cgt gat 1971
 Glu Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp
 560 565 570

5 gag cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc cgt gga 2019
 Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Ser Arg Gly
 575 580 585

10 ggt ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc ggt gga 2067
 Gly Phe Arg Gly Gly Arg Asp Arg Asp Arg Gly Gly Arg Gly Gly
 590 595 600

15 ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc ggt tac 2115
 Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Arg Gly Gly Tyr
 605 610 615

20 cgt ggc gga cgc gac taagagttcg ttttagcttc agctcagggtt ttcgcctgag 2170
 Arg Gly Gly Arg Asp
 620

25 tctggtgctt agctagaaaa atccgttgct ctctctttac tgagagggca acggattttt 2230
 tctgttttct taggctttgg ttcttggggg atcttggggg aggaattcta ggaacttaga 2290

30 gaagtaaatg atggtgcttc gaccgcagca ccacgtgtaa gattctgacc aaagaagaga 2350
 gcattgcgtt gctctctagt cagagtgcga g 2381

35 <210> 2
 <211> 624
 <212> PRT
 <213> Corynebacterium glutamicum

40 Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr
 1 5 10 15
 Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln
 20 25 30
 Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe
 35 40 45

45 Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln
 50 55 60
 Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala Leu Gln Val Ala Asp
 65 70 75 80

50 Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro
 85 90 95

55 Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg
 100 105 110
 Gly Ala His Ile Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu
 115 120 125

000557 BT / AL1

Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp
 130 135 140
 5 Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg
 145 150 155 160
 Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala
 165 170 175
 10 Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn
 180 185 190
 Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile
 195 200 205
 15 Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu
 210 215 220
 Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val
 225 230 235 240
 Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg
 245 250 255
 25 Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg
 260 265 270
 Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val
 275 280 285
 30 Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His
 290 295 300
 Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg
 305 310 315 320
 Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe
 325 330 335
 40 Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr
 340 345 350
 Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn
 355 360 365
 45 Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu
 370 375 380
 Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln
 385 390 395 400
 50 Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln
 405 410 415
 55 Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg
 420 425 430
 Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly
 435 440 445

000557 BT / AL1

Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg
 450 455 460
 5 Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly
 465 470 475 480
 Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn
 485 490 495
 10 Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala
 500 505 510
 Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu
 515 520 525
 15 Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu
 530 535 540
 20 Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg
 545 550 555 560
 Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg
 565 570 575
 25 Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly
 580 585 590
 Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp
 595 600 605
 30 Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp
 610 615 620
 35 <210> 3
 <211> 28
 <212> DNA
 <213> Artificial sequence
 40 <220>
 <223> Description of the artificial sequence: Primer dead
 for2
 45 <400> 3
 gatctagaaa tccgcttcg atgcactc 28
 50 <210> 4
 <211> 28
 <212> DNA
 <213> Artificial sequence
 55 <220>
 <223> Description of the artificial sequence: Primer dead
 int2

000557 BT / AL1

<400> 4

ctaagcttcg acggttgga gttocatt

28

000557 BT / AL1